## SEQUENCE LISTING

#### (1) GENERAL INFORMATION:

(i)	7	זמ	ST.	-	$\sim n$	ידיזא	

- (A) NAME: The University of Leicester
- (B) STREET: University Road
- (C) CITY: Leicester
- (E) COUNTRY: United Kingdom
- (F) POSTAL CODE (ZIP): LE1 7RH

### (ii) TITLE OF INVENTION: Complement Inhibitor

#### (iii) NUMBER OF SEQUENCES: 14

#### (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

#### (2) INFORMATION FOR SEQ ID NO: 1:

#### (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4229 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TCGAGTCAAC	TGCTCCCAGA	TAGATCCAAG	ACATGAGACT	GTCAGCAAGA	ATTATTTGGC	60
TTATATTATG	GACTGTTTGT	GTAGCAGAAG	ATGTAAAGG	TCCTCCTCCA	AGAGAAAATT	120
CAGAAATTCT	CTCAGGTTCG	TGGTCTGAAC	AACTATATTC	AGAAGGCACT	CAGGCAACCT	180
ACAAATGCCG	CCCTGGATAC	CGAACACTTG	GTACTATTGT	AAAAGTATGC	AAGAATGGAG	240
AATGGGTACC	TTCTAACCCA	TCAAGGATAT	GTGGGAAAAG	GCCATGTGGG	CATCCCGGAG	300
ACACACCCTT	TGGGTCCTTT	AGGCTGGCAG	TTGGATCTGA	ATTTGAATTT	GGTGCAAAGG	360
TTGTTTATAC	ATGTGATGAA	GGGTACCAAC	TATTAGGTGA	AATTGATTAC	CGTGAATGTG	420
ATGCAGATGG	GTGGACCAAT	GATATTCCAA	TATGTGAAGT	TGTGAAGTGC	TTGCCAGTGA	480
CAGAACTGGA	GAATGGAAGA	ATTGTGAGTG	GTGCAGCCGA	ACCAGACCAG	GAATATTATT	540
TTGGACAGGT	GGTACGCTTT	GAATGCAACT	CCGGCTTCAA	GATTGAAGGA	CAGAAAGAAA	600
TGCACTGCTC	ATAAAATGGC	CTCTGGAGCA	ATGAAAAGCC	ACAGTGTGTG	GAAATTTCTT	660

720	TACAAGGAGA	GAAACCAGTT	GTATATATCT	AATGGAGATG	ACGAGTTGAA	GCCTGCCACC
780	GGGGATGCTG	CAAAGAAAGA	GTTTTGTGTA	TGTAAGCAAG	ССААТАТААА	ATGAAAGATT
840	TGTTTGACTC	AGAAATGACA	CTTCCTGTGA	AATCCTCAGC	TTCTGGATGG	TCTGCACGGG
900	GATGATGAAA	ACACAGAATT	ACAGGATTAA	TACACACCTC	AAATGGTATC	CATATATTCC
960	TCAAAGTGTA	ATCACCTGTT	CTGCAACCCG	GGCTTCTATC	ATGTAAAAAT	TCAGATATGA
1020	TTTCCACAAT	ACCTTGTGAT	GTAGCTTGAA	GCTCCAAGAT	CTGGATCCCT	CAATTACTGG
1080	GTACCTATAG	CTACTTCCCA	GCCGGAGACC	TATGAAGAAA	ACGTCTGTAT	TCAAACATGG
1140	TCATACTGGG	GCCTTCACAG	GGTTTACAAC	TGTGACAACG	CAGCTATAAC	GAAAGGAGTA
1200	AGGCAATGTA	TCCATGCCTC	AGCCTGAAGT	AATGGGTGGG	TTGCACAGTA	ACTACCTTCG
1260	ATAGAGGGTC	AAGAAGATAT	CATACTGGCA	GGAGAATCTT	TGTGGAATAT	TTTTCCATTA
1320	GATACATATT	AAATGGTCAA	ATAGTCTTCC	CACAGTGGCT	AGTCCAGTGT	AGTCTGCAAA
1380	ACTTGTTCAG	CCGTATCAAG	CCAAATGCGT	TCCCCTCCTC	GAATGGCTGG	ATTGTACAGA
1440	TATGCTCTAA	TGATTATACA	TTTCTGAATC	AATGGGTTTT	AGAAATTGAA	TATCAGATAT
1500	GAAATATCAG	AAATACCGGA	GATATGTAAC	TGTAAACAGG	ACGGTATAGA	ATAGAAAAAC
1560	AAGTCTTGTG	CTCATGCATT	CACCTCGACC	GATGGATGGT	TTGTCTTCAA	GAATAATTAC
1620	AAACTCAATG	CACATGGTTT	AGAATAATAA	TCTATGACTA	ATTTGAGAAT	ATATGCCTGT
1680	ACCAAAGGCT	ATATAAACAT	ATGAAAATGA	CACATTGGAT	CTATGAATGT	ACAAATTAGA
1740	AGAGAATGCA	CTGTTATGAA	GTACACCCTC	GGATGGTCTA	TACTTATGAT	CTATAACATG
1800	TACAAAGTTG	AGAAGTAAAA	TTTTTCCCAG	GACTTAGTTG	GTTACACCAA	GCATTCCCCT
1860	TTAGTGCAAT	TGGAGCAGAT	GACACAGAGT	TGCCGTTCAG	GAGTTTCTCT	GAGATTCGTT
1920	AAATCATGTG	AGGCCAAGTA	CAACGTGTGA	CCTAATTTCC	TGGATGGTCC	GCTACCACTT
1980	GAATACAGCC	AAAAAAAGTT	TAAAGGGAAC	AATGGGGAAA	TGAAATCCCG	ACCAACCTCT
2040	CCCAATAAAA	ACTGAAGGGA	CTAGATTTCT	GATTGCAAAC	GGTGGAATAT	ATGGTGACGT
2100	GAGAGAACAT	CGTTGAGTAT	TGCCGATATG	TGGACAAGGT	TGACGGGAAG	TCCAGTGTGT
2160	CCCTACCATC	ATCTGTCCCT	CTGTCAAGTT	GAGCATGGCT	TCCTGAACTT	GTGGAGACCT
2220	CATGCAGTAG	AATGATTGGA	AAACCTTCAC	ACTTGTACAG	AGTGGAGTTC	ATGGAGATTC
2280	GATCAACTGG	TGTTGCAACA	TTCCTCAATG	TGGACCGAGC	TAGTGGAAGG	TTTTCTGCAT
2340	AAGAATGAAT	TCATCCAAAT	TAGATGCAAT	TCAACTGGCA	AGCCCCGAAG	AGAAGTGTAA

TTAATCATAA	CTTTAGTGTG	AGTTACAGAT	GTAGACAAAA	GCAGGAGTAT	GAACATTCAA	2400
TCTGCATCAA	TGGAAGATGG	GATCCTGAAC	CAAACTGTAC	AAGCAAAAGA	TTCTGCCCTC	2460
CTCCCCGCA	GATTCCAAAT	GCCCAAGTGA	TTGAAACCAC	CGTGAAATAC	TTGGATGGAG	2520
AAAAAGTATC	TGTTCTTTGC	CAAGATGGTT	ACCTAACTCA	GGGCCCAGAA	GAAATGGTGT	2580
GTAAACATGG	AAGGTGGCAG	TCGTTACCAC	GCTGCACGGA	AAAAATTCCA	TGTTCCCAGC	2640
CCCCTAAAAT	TGAACATGGA	TCTATTAAGT	CGCCCAGGTC	CTCAGAAGAG	AGGAGAGATT	2700
TAATTGAGTC	CAGCAGTTAT	GAACACGGAA	CTACATTCAG	CTATTGCTGT	AGAGATGGAT	2760
TCAAGATATC	TGAAGAAAAT	AGGGTAACCT	GCAACATGGG	AAAATGGAGC	TCTCTGCCTC	2820
GTTGTGTTGG	AATACCTTGT	GGACCCCCAC	CTTCAATTCC	TCTTGGTATT	GTTTCTCATG	2880
AACTAGAAAG	TTACCAATAT	GGAGAGGAGG	TTACATACAA	TTGTTCTGAA	GGCTTTGGAA	2940
TTGATGGACC	AGCATTTATT	AAATGTGTAG	GAGGACAGTG	GTCTGAACCT	CCCAAATGCA	3000
TAAAAACTGA	TTGTGACAAC	TTGCCCACAT	TTGAAATTGC	CAAACCGACA	GAAAAGAAAA	3060
AAAAATCATA	CAGGTCAGGA	GAACAAGTGA	CATTCAGATG	TCCACCTCCG	TATCGAATGG	3120
ATGGCTCTGA	CATTGTCACA	TGTGTTAATA	CGAAGTGGAT	TGGACAGCCG	GTATGCAAAG	3180
ATAATTCCTG	TGTGAATCCA	CCACATGTGC	CAAATGCTAC	TATACTAACA	AGGCACAAGA	3240
CTAAATATCC	ATCTGGTGAC	AAAGTACGTT	ATGACTGTAA	TAAACCTTTT	GAATTATTTG	3300
GGGAAGTGGA	AGTGATGTGC	CAAAACGGGA	TTTGGACAGA	ACCACCGAAA	TGCAAAGATT	3360
CAACAGGGAA	ATGTGGGCCT	CCTCCACCTA	TTGACAATGG	AGACATCACC	TCCTTGTCAT	3420
TACCAGTATA	TGCACCATTA	TCATCAGTTG	AATATCAATG	CCAGAACTAT	TATCTACTTA	3480
AGGGAAATAA	GATAGTAACA	TGTAGAAATG	GAAAGTGGTC	TCAGCCACCA	ACCTGCTTAC	3540
ATGCATGTGT	GATACCAGAA	GATATTATGG	AAAAACATAA	TATAGTTCTC	AGATGGAGGG	3600
AAAATGCAAA	GATTTATTCC	CAATCAGGGG	AGAATATTGA	ATTCATGTGT	AAACCTGGAT	3660
ATAGAAAATT	CAGAGGATCA	CCTCCGTTTC	GTACAAAGTG	CATTGAGGGT	CACATCAATT	3720
ATCCCACTTG	TGTATAAAAT	CGCTATACAA	TTATTAGTAA	ACCTTATGGA	TGAGAAATGC	3780
ACATGTATAT	TACTAATACA	GTTTGAATTT	ACATTTAAAT	ATTGTTTAGC	TCATTTCCTC	3840
TAATAAGTAT	ATAAACTTTT	TTTATATGGT	GGTTAATCAG	TAACTTTACA	GACTGTTGCC	3900
ACAAAGCAAG	AACATTACAT	TCAAAACTCC	TAATCCAAAT	ATGATATGTC	CAAGGACAAA	3960
CTATGTCTAA	. GCAAGAAAAT	AAATGTTAGT	TCTTCAATGT	CTGTTTTTAT	TCAGGACCTT	4020
			•			

TCAGATTTTC	TTGGATACCT	TTTGTTAGGT	TCTGATTCAC	AGTGAGTGGA	AGACACACTG	4080
ACTCTGACTT	CAAATTAGTA	TTACTTGCAA	TACATTAACA	ACCAAACTAT	CATAATATCA	4140
CAAATGTATA	CAGCTAATTA	CTGTGTCCTA	CCTTTGTATC	AATAAAGAAA	TCTAAGAAAG	4200
TTCTTGCTTA	АААААААА	АААААААА				4229

## (2) INFORMATION FOR SEQ ID NO: 2:

- . (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 866 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TCGAGTCAAC	TGCTCCCAGA	TAGATCCAAG	ACATGAGACT	GTCAGCAAGA	ATTATTTGGC	60
TTATATTATG	GACTGTTTGT	GTAGCAGAAG	ATTGTAAAGG	TCCTCCTCCA	AGAGAAAATT	120
CAGAAATTCT	CTCAGGTTCG	TGGTCTGAAC	AACTATATTC	AGAAGGCACT	CAGGCAACCT	180
ACAAATGCCG	CCCTGGATAC	CGAACACTTG	GTACTATTGT	AAAAGTATGC	AAGAATGGAG	240
AATGGGTACC	TTCTAACCCA	TCAAGGATAT	GTCGGAAAAG	GCCATGTGGG	CATCCCGGAG	300
ACACACCCTT	TGGGTCCTTT	AGGCTGGCAG	TTGGATCTGA	ATTTGAATTT	GGTGCAAAGG	360
TTGTTTATAC	ATGTGATGAA	GGGTACCAAC	TATTAGGTGA	AATTGATTAC	CGTGAATGTG	420
ATGCAGATGG	GTGGACCAAT	GATATTCCAA	TATGTGAAGT	TGTGAAGTGC	TTGCCAGTGA	480
CAGAACTGGA	GAATGGAAGA	ATTGTGAGTG	GTGCAGCCGA	ACCAGACCAG	GAATATTATT	540
TTGGACAGGT	GGTACGCTTT	GAATGCAACT	CCGGCTTCAA	GATTGAAGGA	CAGAAAGAAA	600
TGCACTGCTC	ATAAAATGGC	CTCTGGAGCA	ATGAAAAGCC	ACAGTGTGTG	GAAATTTCTT	660
GCCTGCCACC	ACGAGTTGAA	AATGGAGATG	GATATAGAAA	ATTCAGAGGA	TCACCTCCGT	720
TTCGTACAAA	GTGCATTGAG	GGTCACATCA	ATTATCCCAC	TTGTGTATAA	AATCGCTATA	780
CAATTATTAG	TAAACCTTAT	GGATGACACT	TTGTTTAGAA	ATGCACATGT	ATATTACTAA	840
TACAGTTTGA	ATTTACATTT	GAAAAA				866

# (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2715 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown-

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

	TCGAGTCAAC	TGCTCCCAGA	TAGATCCAAG	ACATGAGACT	GTCAGCAAGA	ATTATTTGGC	60
	TTATATTATG	GACTGTTTGT	GTAGCAGAAG	ATTGTAAAGG	TCCTCCTCCA	AGAGAAAATT	120
	CAGAAATTCT	CTCAGGTTCG	TGGTCTGAAC	AACTATATTC	AGAAGGCACT	CAGGCAACCT	180
	ACAAATGCCG	CCCTGGATAC	CGAACACTTG	GTACTATTGT	AAAAGTATGC	AAGAATGGAG	240
	AATGGGTACC	TTCTAACCCA	TCAAGGATAT	GTCGGAAAAG	GCCATGTGGG	CATCCCGGAG	300
	ACACACCCTT	TGGGTCCTTT	AGGCTGGCAG	TTGGATCTGA	ATTTGAATTT	GGTGCAAAGG	360
	TTGTTTATAC	ATGTGATGAA	GGGTACCAAC	TATTAGGTGA	AATTGATTAC	CGTGAATGTG	420
	ATGCAGATGG	GTGGACCAAT	GATATTCCAA	TATGTGAAGT	TGTGAAGTGC	TTGCCAGTGA	480
	CAGAACTGGA	GAATGGAAGA	ATTGTGAGTG	GTGCAGCCGA	ACCAGACCAG	GAATATTATT	540
	TTGGACAGGT	GGTACGCTTT	GAATGCAACT	CCGGCTTCAA	GATTGAAGGA	CAGAAAGAAA	600
	TGCACTGCTC	ATAAAATGGC	CTCTGGAGCA	ATGAAAAGCC	ACAGTGTGTG	TTGAAACCTT	660
	GTGATTTTCC	ACAATTCAAA	CATGGACGTC	TGTATTATGA	AGAAAGCCGG	AGACCCTACT	720
	TCCCAGTACC	TATAGGAAAG	GAGTACAGCT	ATAACTGTGA	CAACGGGTTT	ACAACGCCTT	780
	CACAGTCATA	CTGGGACTAC	CTTCGTTGCA	CAGTAAATGG	GTGGGAGCCT	GAAGTTCCAT	840
	GCCTCAGGCA	ATGTATTTTC	CATTATGTGG	AATATGGAGA	ATCTTCATAC	TGGCAAAGAA	900
	GATATATAGA	GGGTCAGTCT	GCAAAAGTCC	AGTGTCACAG	TGGCTATAGT	CTTCCAAATG	960
	GTCAAGATAC	ATATTATTGT	ACAGAGAATG	GCTGGTCCCC	TCCTCCCAAA	TGCGTCCGTA	1020
	TCAAGACTTG	TTCAGTATCA	GATATAGAAA	TTGAAAATGG	GTTTTTTTCT	GAATCTGATT	1080
	ATACATATGC	TCTAAATAGA	AAAACACGGT	ATAGATGTAA	ACAGGGATAT	GTAACAAATA	1140
	CCGGAGAAAT	ATCAGGAATA	ATTACTTGTC	TTCAAGATGG	ATGGTCACCT	CGACCCTCAT	1200
	GCATTAAGTC	TTGTGATATG	CCTGTATTTG	AGAATTCTAT	GACTAAGAAT	AATAACACAT	1260
	GGTTTAAACT	CAATGACAAA	TTAGACTATG	AATGTCACAT	TGGATATGAA	AATGAATATA	1320
	AACATACCAA	AGGCTCTATA	ACATGTACTT	ATGATGGATG	GTCTAGTACA	CCCTCCTGTT	1380
	ATGAAAGAGA	ATGCAGCATT	CCCCTGTTAC	ACCAAGACTT	AGTTGTTTTT	CCCAGAGAAG	1440
	TAAAATACAA	AGTTGGAGAT	TCGTTGAGTT	TCTCTTGCCG	TTCAGGACAC	AGAGTTGGAG	1500
	CAGATTTAGT	GCAATGCTAC	CACTTTGGAT	GGTCCCCTAA	TTTCCCAACG	TGTGAAGGCC	1560
•	AAGTAAAATC	ATGTGACCAA	CCTCTTGAAA	TCCCGAATGG	GGAAATAAAG	GGAACAAAAA	1620

AAGTTGAATA	CAGCCATGGT	GACGTGGTGG	AATATGATTG	CAAACCTAGA	TTTCTACTGA	1680
AGGGACCCAA	TAAAATCCAG	TGTGTTGACG	GGAAGTGGAC	AAGGTTGCCG	ATATGCGTTG	1740
AGTATGAGAG	AACATGTGGA	GACCTTCCTG	AACTTGAGCA	TGGCTCTGTC	AAGTTATCTG	1800
TCCCTCCCTA	CCATCATGGA	GATTCAGTGG	AGTTCACTTG	TACAGAAACC	TTCACAATGA	1860
TTGGACATGC	AGTAGTTTTC	TGCATTAGTG	GAAGGTGGAC	CGAGCTTCCT	CAATGTGTTG	1920
CAACAGATCA	ACTGGAGAAG	TGTAAAGCCC	CGAAGTCAAC	TGGCATAGAT	GCAATTCATC	1980
CAAATAAGAA	TGAATTTAAT	CATAACTTTA	GTGTGAGTTA	CAGATGTAGA	CAAAAGCAGG	2040
agtatgaaca	TTCAATCTGC	ATCAATGGAA	GATGGGATCC	TGAACCAAAC	TGTACAAGCA	2100
AAAGATTCTG	CCCTCCTCCC	CCGCAGATTC	CAAATGCCCA	AGTGATTGAA	ACCACCGTGA	2160
AATACTTGGA	TGGAGAAAA	GTATCTGTTC	TTTGCCAAGA	TGGTTACCTA	ACTCAGGGCC	2220
CAGAAGAAAT	GGTGTGTAAA	CATGGAAGGT	GGCAGTCGTT	ACCACGCTGC	ACGGAAAAA	2280
TTCCATGTTC	CCAGCCCCCT	AAAATTGAAC	ATGGATCTAT	TAAGTCGCCC	AGGTCCTCAG	2340
AAGAGAGGAG	AGATTTAATT	GAGTCCAGCA	GTTATGAACA	CGGAACTACA	TTCAGCTATT	2400
GCTGTAGAGA	TGGATTCAAG	ATATCTGAAG	AAAATAGGGT	AACCTGCAAC	ATGGGAAAAT	2460
GGAGCTCTCT	GCCTCGTTGT	GTTGGAATAC	CTTGTGGACC	CCCACCTTCA	ATTCCTCTTG	2520
GTATTGTTTC	TCATGAACTA	GAAAGTTACC	AATATGGAGA	GGAGGTTACA	TACAATTGTT	2580
CTGAAGGCTT	TGGAATTGAT	GGACCAGCAT	TTATTAAATG	TGTAGGAGGA	CAGTGGTCTG	2640
AACCTCCCAA	ATGCATAAAA	ACTGATTGTG	ACAACTTGCC	CACATTTGAA	ATTGCCAAAC	2700
CGACAGAAAA	GAAAA					2715

## (2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1532 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

60	ATTATTTGGC	GTCAGCAAGA	ACATGAGACT	TAGATCCAAG	TGCTCCCAGA	TCGAGTCAAC
120	AGAGAAAATT	TCCTCCTCCA	ATTGTAAAGG	GTAGCAGAAG	GACTGTTTGT	TTATATTATG
180	CAGGCAACCT	AGAAGGCACT	AACTATATTC	TGGTCTGAAC	CTCAGGTTCG	CAGAAATTCT
240	AAGAATGGAG	AAAAGTATGC	GTACTATTGT	CGAACACTTG	CCCTGGATAC	· ACAAATGCCG

AATGGGTACC	TTCTAACCCA	TCAAGGATAT	GTCGGAAAAG	GCCATGTGGG	CATCCCGGAG	300
ACACACCCTT	TGGGTCCTTT	AGGCTGGCAG	TTGGATCTGA	ATTTGAATTT	GGTGCAAAGG	360
TTGTTTATAC	ATGTGATGAA	GGGTACCAAC	TATTAGGTGA	AATTGATTAC	CGTTATCGAA	420
TGGATGGCTC	TGACATTGTC	ACATGTGTTA	ATACGAAGTG	GATTGGACAG	CCGGTATGCA	480
AAGATAATTC	CTGTGTGAAT	CCACCACATG	TGCCAAATGC	TACTATACTA	ACAAGGCACA	540
AGACTAAATA	TCCATCTGGT	GACAAAGTAC	GTTATGACTG	TAATAAACCT	TTTGAATTAT	600
TTGGGGAAGT	GGAAGTGATG	TGCCAAAACG	GGATTTGGAC	AGAACCACCG	AAATGCAAAG	660
ATTCAACAGG	GAAATGTGGG	CCTCCTCCAC	CTATTGACAA	TGGAGACATC	ACCTCCTTGT	720
CATTACCAGT	ATATGCACCA	TTATCATCAG	TTGAATATCA	ATGCCAGAAC	TATTATCTAC	780
TTAAGGGAAA	TAAGATAGTA	ACATGTAGAA	ATGGAAAGTG	GTCTCAGCCA	CCAACCTGCT	840
TACATGCATG	TGTGATACCA	GAAGATATTA	TGGAAAAACA	TAATATAGTT	CTCAGATGGA	900
GGGAAAATGC	AAAGATTTAT	TCCCAATCAG	GGGAGAATAT	TGAATTCATG	TGTAAACCTG	960
GATATAGAAA	ATTCAGAGGA	TCACCTCCGT	TTCGTACAAA	GTGCATTGAG	GGTCACATCA	1020
ATTATCCCAC	TTGTGTATAA	AATCGCTATA	CAATTATTAG	TAAACCTTAT	GGATGAGAAA	1080
TGCACATGTA	TATTACTAAT	ACAGTTTGAA	TTTACATTTA	AATATTGTTT	AGCTCATTTC	1140
CTCTAATAAG	TATATAAACT	TTTTTTTTT	GGTGGTTAAT	CAGTAACTTT	ACAGACTGTT	1200
GCCACAAAGC	AAGAACATTA	CATTCAAAAC	TCCTAATCCA	AATATGATAT	GTCCAAGGAC	1260
AAACTATGTC	TAAGCAAGAA	AATAAATGTT	AGTTCTTCAA	TGTCTGTTTT	TATTCAGGAC	1320
CTTTCAGATT	TTCTTGGATA	CCTTTTGTTA	GGTTCTGATT	CACAGTGAGT	GGAAGACACA	1380
CTGACTCTGA	CTTCAAATTA	GTATTACTTG	CAATACATTA	ACAACCAAAC	TATCATAATA	1440
TCACAAATGT	ATACAGCTAA	TTACTGTGTC	CTACCTTTGT	ATCAATAAAG	AAATCTAAGA	1500
AAGTTCTTGC	TTAAAAAAAA	AAAAAAAA	AA			1532

#### (2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

(2)	INFO	RMATI	ON F	OR S	EQ I	D NO	: 6:										
	(i)	(B) (C)	LEN TYP STR	GTH: E: n ANDE	RACT 33 ucle DNES Y: u	base ic a S: s	pai: cid ingl	rs							·		
	(xi)	SEQU	ENCE	DES	CRIP	TION	: SE	Q ID	NO:	6:							
GGC	GCCG	CT CA	AATC	TTCT	GAG.	ATAT.	AGG	AGA									33
(2)	INFO	RMATI	ON F	OR S	EQ I	D NO	: 7:										
	(i)	(B)	LEN TYP STR	GTH: E: n ANDE	RACT 33 ucle DNES Y: u	base ic a S: s	pai: cid ingl	rs									
	(xi)	SEQU	ENCE	DES	CRIP	TION	: SE	Q ID	NO:	7:							
GGC	GCCG	CT CA	TTTA	ATCC	TTA	AAGG	TGA	GTA									33
(2)	INFO	RMATI	ON F	OR S	EQ I	D NO	: 8:										
	(i)	(B) (C)	LEN TYP STR	GTH: E: n ANDE	RACT 33 ucle DNES Y: u	base ic a S: s	pai cid ingl	rs									
	(xi)	SEQU	ENCE	DES	CRIP	TION	: SE	QID	NO:	8:							
GGC	GCCG	CT CA	TACI	GGAA	AGT	ATGG	TCT	ACG									33
(2)	INFO	RMATI	ON F	OR S	EQ I	D NC	): 9:										
	(i)	(B)	LEN TYP STR	IGTH: PE: & RANDE	ARACT 207 Amino EDNES SY: u	ami aci S:	.no a .d		<b>.</b>								
	(xi)	SEQU	JENCI	E DES	SCRIE	OIT	1: SE	EQ II	NO:	9:							
	Glu 1	Asp	Cys	Asn	Glu 5	Leu	Pro	Pro	Arg	Arg 10	Asn	Thr	Glu	Ile	Leu 15	Thr	
	Gly	Ser	Trp	Ser 20	Asp	Gln	Thr	Tyr	Pro 25	Glu	Gly	Thr	Gln	Ala 30	Ile	Tyr	

Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys 35 40 45

Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys 50 55 60

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu 70 75 80

Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys 85 90 95

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp 100 105 110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
115 120 125

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met 130 135 140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys
145 150 155 160

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp 165 170 175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys 180 185 190

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile 195 200 205

#### (2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 265 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
1 5 10 15

Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr
20 25 30

Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys 35 40 45

Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys 50 55 60

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu 65 70 75 80

Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp 100 105 110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met 130 135 140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys 145 150 155

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp 165 170 175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile 195 200 205

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu 210 215 220

Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro

Leu Pro Ser Cys Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile Pro Asn 245 250 255

Gly Asp Tyr Ser Pro Leu Arg Ile Lys 260 265

## (2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 329 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: unknown
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
1 5 10 15

Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr 20 25 30

Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys 90 Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp 100 Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys 120 Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys 150 Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp 170 Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys 180 Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile 200 Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro 230 225 Leu Pro Ser Cys Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile Pro Asn 250 Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile Thr Tyr Gln Cys Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly Asn Thr 280 Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu 300 Lys Pro Cys Asp Tyr Pro Asp Ile Lys His Gly Gly Leu Tyr His Glu

315

Asn Met Arg Arg Pro Tyr Phe Pro Val

305

(2)	INFORMATION	FOR	SEQ	ID	NO:	12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

## CCTCCTCCTG GAAATGTTAG AAGCTTAAGA TG

32

- (2) INFORMATION FOR SEQ ID NO: 13:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 29 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: unknown
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

# CCTCTAGATT ACTTGATACG GACGCATTT

29

- (2) INFORMATION FOR SEQ ID NO: 14:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 428 amino acids
    - (B) TYPE: amino acid
    - (C) STRANDEDNESS:
    - (D) TOPOLOGY: unknown
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
  - Glu Asp Cys Lys Gly Pro Pro Pro Arg Glu Asn Ser Glu Ile Leu Ser
  - Gly Ser Trp Ser Glu Gln Leu Tyr Ser Glu Gly Thr Gln Ala Thr Tyr 20 25 30
  - Lys Cys Arg Pro Gly Tyr Arg Thr Leu Gly Thr Ile Val Lys Val Cys
    35 40 45
  - Lys Asn Gly Glu Trp Val Pro Ser Asn Pro Ser Arg Ile Cys Arg Lys
    50 55 60
  - Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Ser Phe Arg Leu 65 70 75 80
  - Ala Val Gly Ser Glu Phe Glu Phe Gly Ala Lys Val Val Tyr Thr Cys 85 90 95
  - Asp Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asp Tyr Arg Glu Cys Asp

110 105 100 Ala Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys 120 Leu Pro Val Thr Glu Leu Glu Asn Gly Arg Ile Val Ser Gly Ala Ala 135 Glu Pro Asp Gln Glu Tyr Tyr Phe Gly Gln Val Val Arg Phe Glu Cys 145 Asn Ser Gly Phe Lys Ile Glu Gly Gln Lys Glu Met His Cys Ser Glu 170 Asn Gly Leu Trp Ser Asn Glu Lys Pro Gln Cys Val Glu Ile Ser Cys Leu Pro Pro Arg Val Glu Asn Gly Asp Gly Ile Tyr Leu Lys Pro Val 200 195 Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Lys Gln Gly Phe Val 215 Tyr Lys Glu Arg Gly Asp Ala Val Cys Thr Gly Ser Gly Trp Asn Pro 225 Gln Pro Ser Cys Glu Glu Met Thr Cys Leu Thr Pro Tyr Ile Pro Asn 250 Gly Ile Tyr Thr Pro His Arg Ile Lys His Arg Ile Asp Asp Glu Ile 270 Arg Tyr Glu Cys Lys Asn Gly Phe Tyr Pro Ala Thr Arg Ser Pro Val Ser Lys Cys Thr Ile Thr Gly Trp Ile Pro Ala Pro Arg Cys Ser Leu 295 Lys Pro Cys Asp Phe Pro Gln Phe Lys His Gly Arg Leu Tyr Tyr Glu 305 Glu Ser Arg Arg Pro Tyr Phe Pro Val Pro Ile Gly Lys Glu Tyr Ser Tyr Tyr Cys Asp Asn Gly Phe Thr Thr Pro Ser Gln Ser Tyr Trp Asp 345 Tyr Leu Arg Cys Thr Val Asn Gly Trp Glu Pro Glu Val Pro Cys Leu Arg Gln Cys Ile Phe His Tyr Val Glu Tyr Gly Glu Ser Ser Tyr Trp 375 Gln Arg Arg Tyr Ile Glu Gly Gln Ser Ala Lys Val Gln Cys His Ser 390

**x**, **y**,

Gly Tyr Ser Leu Pro Asn Gly Gln Asp Thr Tyr Tyr Cys Thr Glu Asn 405 410

Gly Trp Ser Pro Pro Pro Lys Cys Val Arg Ile Lys
420 425

rFH1.0

1

Figure 1							
	10	20	30 -18	40	50	60	
togagto	aactgctccc	agatagat	.ccaagac <u>ATG</u> A	GACTGTCAG	CAAGAATTATI	TGGC	rFH4.3
			.ccaagac <u>ATG</u> A				rFH2.7
togagto	aactgctccc	agatagat	ccaagac <u>ATG</u> A	GACTGTCAG	CAAGAATTATI	TGGC	rFH1.8
togagto	aactgctccc	agatagat	ccaagac <u>ATG</u> A	GACTGTCAG	CAAGAATTATT	TGGC	rFH1.0
			SCR1				
	70	80	+1 90	100	110	120	
TTATATTA	ATGGACTGTT	TGTGTAGC	a <u>gaa</u> gattgta	AAGGTCCTC	CTCCAAGAGAA	AATT	rFH4.3
TTATATT	ATGGACTGTT	TGTGTAGC.	a <u>gaa</u> gattgta	AAGGTCCTC	CTCCAAGAGAA	AATT	rFH2.7
TTATATTA	ATGGACTGTT	TGTGTAGC	a <u>gaa</u> gattgta	AAGGTCCTC	CTCCAAGAGAA	AATT	rFH1.8
TTATATTA	ATGGACTGTT	TGTGTAGC.	A <u>GAA</u> GATTGTA	AAGGTCCTC	CTCCAAGAGAA	AATT	rFH1.0
	130	140	150	160	170	180	
			TGAACAACTAT				rFH4.3
CAGAAATT	CTCTCAGGT	TCGTGGTC'	TGAACAACTAT	ATTCAGAAG	GCACTCAGGCA	ACCT	rFH2.7
CAGAAATT	CTCTCAGGT	TCGTGGTC	TGAACAACTAT	ATTCAGAAG	GCACTCAGGCA	ACCT	rFH1.8
CAGAAATI	CTCTCAGGT	TCGTGGTC'	TGAACAACTAT	ATTCAGAAG	GCACTCAGGCA	ACCT	rFH1.0
	190	200	210	220	230	240	
			ACTTGGTACTA				rFH4.3
ACAAATGO	CCCCTGGA	TACCGAAC	ACTTGGTACTA	TTGTAAAAG	TATGCAAGAAT	GGAG	rFH2.7
ACAAATGO	CCCCCTGGA	TACCGAAC.	ACTTGGTACTA	TTGTAAAAG	TATGCAAGAAT	GGAG	rFH1.8
ACAAATGO	CCGCCCTGGA	TACCGAAC	ACTTGGTACTA	TTGTAAAAG	TATGCAAGAAT	GGAG	rFH1.0
			sc	R2a			
	250	260	270	280	290	300	
AATGGGT	ACCTTCTAAC	CCATCAAG	GATATGTCGGA	AAAGGCCAT	GTGGGCATCCC	GGAG	rFH4.3
AATGGGT	ACCTTCTAAC	CCATCAAG	GATATGTCGGA	AAAGGCCAT	GTGGGCATCCC	GGAG	rFH2.7
			GATATGTCGGA				rFH1.8
			GATATGTCGGA				rFH1.0
.4.10001.							
	310	320	330	340	350	360	
ACACACC	-		GGCAGTTGGAT	CTGAATTTC	AATTTGGTGCA	AAGG	rFH4.3
			GGCAGTTGGAT				rFH2.7
ACACACC							१ स्मिन

ACACACCCTTTGGGTCCTTTAGGCTGGCAGTTGGATCTGAATTTGAATTTGGTGCAAAGG

		SCR25					
	370	380	390	400	410	420	
TTGTTTAT	ACATGTGATG	AAGGGTACCA	ACTATTAGGT	GAAATTGATT.	ACCGTGAATG	rG rFH4	4.3
TTGTTTAT	ACATGTGATG	AAGGGTACCA	ACTATTAGGT	GAAATTGATT	ACCGTGAATGT	rg rfH2	2.7
TTGTTTAT	ACATGTGATG	AAGGGTACCA	ACTATTAGGT	GAAATTGATT	ACCGT	- rFH1	L.8
TTGTTTAT	ACATGTGATG	AAGGGTACCA	ACTATTAGGT	GAAATTGATT	ACCGTGAATGI	G rFH1	L. 0
			SCR3				
	430	440	450	460	470	480	
ATGCAGAT	GGGTGGACCA	ATGATATTCC.	AATATGTGAA	GTTGTGAAGT(	ECTTGCCAGTG	A rFH4	3
ATGCAGAT	GGGTGGACCA	ATGATATTCC	AATATGTGAA(	GTTGTGAAGT	CTTGCCAGTG	A rFH2	. 7
						- rFH1	8
ATGCAGAT	GGGTGGACCA	ATGATATTCC	AATATGTGAA	TTGTGAAGT	SCTTGCCAGTG	A rFH1	0
	490	500	510	520	530	540	
CAGAACTG					GGAATATTAT	T rFH4	. 3
					GGAATATTAT		. 7
						- rFH1	. 8
CAGAACTG	GAGAATGGAAG	BAATTGTGAG	rggtgcagcc	AACCAGACCA	GGAATATTAT	T rFH1	. 0
CAGARC 1 C	JACIBA COIZA						
	550	560	570	580	590	600	
<b>ፕፕሮር</b> ΔርΔር					ACAGAAAGAA	A rFH4	. 3
					ACAGAAAGAA		. 7
						- rFH1	. 8
TTGGACAG	╌ ⋜Ͳ⋶ĠͲϷĊĠĊͲჼ	TTGAATGCAA	TTCCGGCTTC	AGATTGAAGG	ACAGAAAGAA	A rFH1	. 0
11donard	JIGGIACGCI.						
					SCR4		
	610	620	630	640		660	
ייים אייים מייים מייים	•				GGAAATTTCT		. 3
					:G		
IGCACIGC	ICATAAAATG	3CC1C1GGAG	CAAAAD IAA	CACAGIGIGI		- rFH1	
		2000000000000	CD DTCD D D D D C		GGAAATTTCT		
TGCACTGC	TCATAAAAIG	JCC I C I GGAG	CAAIGAAAAG	_CACAGIGIG	GGAAATITCI		
					4	=00	
					710		
					TTACAAGGAG		
						- rFH1	
GCCTGCCA	.CCACGAGTTG	AAAATGGAGA	T			- rFH1	0

# - 3/15 -

	730	740	750	760	770	780	
ATGAAAG	GATTCCAATA	TAAATGTAAG	CAAGGTTTTC	TGTACAAAGA	AAGAGGGGAT	GCTG	rFH4.3
							rFH2.7
							rFH1.8
							rFH1.0
				SCR5			
	790	800		820	830	840	
TCTGCAC	GGGTTCTGG <i>I</i>	ATGGAATCCT	CAGCCTTCCT	GTGAAGAAAT	GACATGTTTG		rFH4.3
							rFH2.7
							rFH1.8
							rFH1.0
	850	860	870	880	890	900	•
CATATAT	TCCAAATGGT	PATCTACACA(	CCTCACAGGA	TTAAACACAG	AATTGATGAT	GAAA	rFH4.3
							rFH2.7
							rFH1.8
					<b></b>		rFH1.0
				940			
TCAGATA	TGAATGTAA	AAATGGCTTC'	ratcctgcaa	CCCGATCACC	TGTTTCAAAG		
							rFH2.7
							rFH1.8
							rFH1.0
				SCR6			
	970	980	990	1000	1010	1020	)
CAATTAC	TGGCTGGAT	CCTGCTCCA	AGATGTAGCI	TGAAACCTTG	TGATTTTCCA	CAAT	rFH4.3
			T	TGAAACCTTG	TGATTTTCCA	CAAT	rFH2.7
							rFH1.8
							rFH1.0
	1030	1040	1050	1060	1070	1080	0
TCDDDC				AGACCCTACTI			rFH4.3
				AGACCCTACTT			rFH2.7
				<del></del> -			rFH1.8
,							rFH1.0

	1090	1100	1110	1120	1130	1140
GAAAGGA	GTACAGCTA	TAACTGTGAC.	AACGGGTTTA	CAACGCCTTC	ACAGTCATAC	TGGG rFH4.3
		TAACTGTGAC				
						rFH1.8
						rFH1.0
					SCR7	
	1150	1160	1170	1180	1190	1200
ACTACCT	TCGTTGCAC	AGTAAATGGG	rgggagcctg	AAGTTCCATG	CCTCAGGCAA	TGTA rFH4.3
ACTACCT	TCGTTGCAC	AGTAAATGGG	rgggagcctg	AAGTTCCATG	CCTCAGGCAA	TGTA rFH2.7
			_,			rFH1.8
						rFH1.0
	1210	1220	1230	1240	1250	1260
TTTTCCA'	TTATGTGGA	ATATGGAGAA:	CTTCATACT	GGCAAAGAAG	ATATATAGAG	GGTC rFH4.3
TTTTCCA	TTATGTGGA	ATATGGAGAA:	CTTCATACT	GGCAAAGAAG.	ATATATAGAG	GGTC rFH2.7
						rFH1.8
						rFH1.0
	1270	1280	1290	1300	1310	1320
		GTGTCACAGT(				
AGTCTGC.	AAAAGTCCA	GTGTCACAGT	GGCTATAGTC	TTCCAAATGG	TCAAGATACA'	TATT rFH2.7
						rFH1.8
						rFH1.0
					SCRB	
	1330	1340	1350	1360	1370	1380
ATTGTAC	AGAGAATGG	CTGGTCCCCT	CCTCCCAAAT	GCGTCCGTAT	CAAGACTTGT	TCAG rFH4.3
		CTGGTCCCCT				
						rFH1.0
	1390	1400	1410	1420	1430	1440
татсаси						CTAA rFH4.3
		ITGAAAATGGG				
						rFH1.8
						rFH1.0

	1450	1460	1470	1480	1490	1500
3 M3 C3 3 3 3			- GGGATATGTA	ACAAATACCG	gagaaatatc <i>a</i>	G rFH4.3
					gagaaatatca	
ATAGAAAA	ACACGGIAIA					- rFH1.8
						rFH1.0
				•		
					SCR9	
	1510	1520	1530	1540	1550	1560
ሮአ አሞአ አጥጥ			GTCACCTCGA	CCTCATGCA'	TAAGTCTTGT	G rFH4.3
					TAAGTCTTGT	
GAATAATT	ACTIGICITES					- rFH1.8
						- rFH1.0
	3.570	1580	1590	1600	1610	1620
	1570				TTAAACTCAAT	G rFH4.3
					rtaaactcaat	
ATATGCCT	GTATTTGAGA	AIICIAIGAC	IANGAMITATI			- rFH1.8
						- rFH1.0
	1630	1640	1650	1660	1670	1680
מראאמיים		GTCACATTGG	ATATGAAAAT	GAATATAAAC	ATACCAAAGGC	rFH4.3
ACAAATTA	GACTATGAAT	GTCACATTGG	ATATGAAAAT	GAATATAAAC	ATACCAAAGGC	rFH2.7
MCMM II						- rFH1.8
						- rFH1.0
					SCR10	
	1690	1700	1710	1720	1730	1740
CC 3 C 3 C 3				TCCTGTTATG	AAAGAGAATG	CA rFH4.3
CTATAACA	AIGIACITAIG	ATGGATGGT(	TAGTACACCC	TCCTGTTATG	AAAGAGAATG	CA rFH2.7
CTATAACA	TGTACTTAIG	AIGGAIGGIC	IAGIACACC			rFH1.8
						rFH1.0
			4.776	1780	1790	1800
					1790	
GCATTCC	CCTGTTACAC	CAAGACTTAG'	TTGTTTTTCC	AGAGAAGTA	AATACAAAGT	TC TEH2 7
GCATTCC	CCTGTTACAC	CAAGACTTAG	TTGTTTTTCC	LAGAGAAGTA	-MMINCHMAGI	TG rFH2.7
						rrmi.v

	1810	1820	1830	1840	1850	1860	
GAGATTCG	TTGAGTTTCI	CTTGCCGTT	CAGGACACAG	AGTTGGAGCA	GATTTAGTGC	AAT rF	H4.3
					GATTTAGTGC		H2.7
							H1.8
						rFI	H1.0
				•			
				so	R11		
	1870	1880	1890	1900	1910	1920	
CTACCAC	TTTGGATGGT	CCCCTAATTI	CCCAACGTGT	GAAGGCCAA	GTAAAATCATG	TG rFF	14.3
					TAAAATCATO		12.7
							11.8
							11.0
	1930	1940	1950	1960	1970	1980	
ACCAACCT	CTTGAAATCC	CGAATGGGGA	AATAAAGGGA	ACAAAAAA	GTTGAATACAG	CC rFF	14.3
					GTTGAATACAG		12.7
							11.8
							11.0
	1990	2000	2010	2020	2030	2040	
тсстсьс				CTACTGAAG	GGACCCAATA	AA rFI	14.3
					GGACCCAATA!		12.7
							H1.8
							H1.0
				SCR1:	2		
	2050	2060	2070		2090	2100	
	2050				TATGAGAGAA		H4.3
TCCAGTGT	rgrigacige	AGIGGACAA	CCTTCCCGAT	ATGCGTTGAG	TATGAGAGAA	CAT rF	H2.7
TCCAGTG							H1.8
						_	H1.0
			•				
		2120		2140			774 7
	CCTTCCTGAA	CTTGAGCATG	GCTCTGTCAA	GTTATCTGT	CCTCCCTACC	ATC rF	'H4.3
	CCTTCCTGAA	CTTGAGCATG	GCTCTGTCAA	GTTATCTGT		ATC rF	H2.7
	CCTTCCTGAA	CTTGAGCATG	GCTCTGTCAA	GTTATCTGT	CCTCCCTACC	ATC rF	H4.3 H2.7 H1.8

	2170	2180	2190	2200	2210	2220
ATGGAGAT	TCAGTGGAGT	TCACTTGTAC	AGAAACCTTC	ACAATGATTO	GACATGCAGT	AG rFH4.3
					GACATGCAGT.	
						rFH1.8
						rFH1.0
					SCR13	
	2230		2250	2200		2280
					CAGATCAACT	
					CAGATCAACT	
						rFH1.0
						0240
	2290		2310			
agaagtgt	'AAAGCCCCGA	AGTCAACTGG	CATAGATGCA	ATTCATCCAA	ATAAGAATGA	AI IFA4.3
					ATAAGAATGAI	
						rFH1.0
						IPHI.O
	2350	2360	2370	2380	2390	2400
ምም እ አምሮ እ <b>ጥ</b>					TATGAACATTC	AA rFH4.3
					TATGAACATTC	
TIAAICAI	AACIIIAGIC					rFH1.8
						rFH1.0
				SCRI	.4	
	2410	2420	2430	2440	2450	2460
<b>יירייביר</b> איינ			ACCAAACTGI	TACAAGCAAA	AGATTCTGCCC	TC rFH4.3
TCTCCATC	TA ATGGA AGA'	rGGGATCCTG	ACCAAACTGT	racaagcaaa	AGATTCTGCCC	TC rFH2.7
10100011						
						rFH1.0
	2470	2480	2490	2500	2510	2520
CTCCCC				CACCGTGAAA	TACTTGGATGG	AG rFH4.3
					TACTTGGATGG	
						rFH1.8
						rFH1.0

	2530	2540	2550	2560	2570	2580
AAAAAGTA	TCTGTTCTTI	CCCAAGATGO	TTACCTAAC	rcagggccca	GAAGAAATGG?	rgt rFH1.8
					gaagaaatgg:	
						rFH4.3
						rFH1.0
				·		
				SCR15		
	2590	2600	2610	2620	2630	2640
<b>ር</b> ሞአአአሮአጥ			ACGCTGCAC		CATGTTCCC	
					CATGTTCCC	
GTAAACAI	GGAAGGIGGC	AGICOITAC				rFH1.8
			·			rFH1.0
		2662	2670	2680	2690	2700
			2670		JAGAGGAGAGA	
CCCCTAAA	ATTGAACATG				eagaggagag <i>i</i>	
						rFH1.0
						11111.0
					0.550	2760
	2710	2720	2730		2750	
					rgtagagatg(	
TAATTGAG	TCCAGCAGTI	TATGAACACG	SAACTACATT	CAGCTATTGC'	rgtagagatg(	
						rFH1.8
	. <b></b>					rFH1.0
	2770	2780	2790	2800	2810	2820
TCAAGAT	ATCTGAAGAA	AATAGGGTAA	CCTGCAACAT	GGGAAAATGG	AGCTCTCTGC	CTC rFH4.3
					AGCTCTCTGC	
						rFH1.8
						rFH1.0
	SCR16	2042	2052	2860	2870	2880
	2830	2840	2850	_		
					ATTGTTTCTC	
GTTGTGT	TGGAATACCT	TGTGGACCCC	CACCTTCAA:	"rccrcrrgg"	TATTGTTTCTC	AIG FFH2.7
						rFH1.0

	2890	2900	2910	2920	2930	2940	
አ ለ ርምክ ር፡ አ አ			GGTTACATAC	AATTGTTCTG	AAGGCTTTGG	AA rFH4	. 3
TWC I WGWY	ACTUACCA AT	ATGGAGAGGA	GGTTACATAC	AATTGTTCTG	AAGGCTTTGG	AA rFH2	.7
AACIAGAA	AGIIACCAII					rFH1	. 8
							. 0
						•-	
		2000	2970	2980	2990	3000	
	2950	2360 mm	'AGGAGGACAG	TGGTCTGAAC	CTCCCAAATG	CA rFH4	. 3
TTGATGGA	.CCAGCATTA	TTAAATGIGI	'AGGAGGACAG 'AGGAGGACAG	TGGTCTGAAC	CTCCCAAATG	CA rFH2	.7
rtgatgga	.CCAGCATTTA	TTAAATGIGI				rFH1	. 8
SCR17				2040	3050	3060	
	3010	3020	3030	3040	2020	aa rFH4	. 3
raaaaact	GATTGTGACA	ACTTGCCCAC	ATTTGAAATT	GCCAAACCGA	CACAAAAAAAA	AA rFH2	. 7
raaaaact	GATTGTGACA	ACTTGCCCAC	ATTTGAAATT	GCCAAACCGA		rFH1	. 8
						rFH1	
						11111	
						2222	
	3070	3080	3090	3100	3110	3120	•
AAAAATCA			rgacattcag <i>i</i>			GG IFH4	
						rFH2	
					TATCGAAT	GG rFH1	8
						rFH1	0
					•		
	3130	3140	3150	3160	3170	3180	
אתיביביתיני	TGACATTGTC	ACATGTGTTA	ATACGAAGTG	JATTGGACAG	CCGGTATGCA	AAG rFH4	1.3
						rFH2	2.7
ATCCCTC	ብር ፓ ር <u>ያ</u> ብሔር ውር -	ACATGTGTTA	ATACGAAGTG	GATTGGACAG	CCGGTATGCA	AAG rFH1	1.8
AIGGCIC	IGACATIGIC					rFHI	1.0
SCR18		2202	3210	3220	3223	3240	
	3190	3200	3210 STGCCAAATGC	שב ב 22.0 מידים בידים בידים	ACAAGGCACA	AGA rFH	4.3
		CCACCACATG	FIGUCAAATGU			rFH	
ATAATTO	CTGTGTGAAI	CCACCACATO	ETGCCAAATGC	. IMCIMINCIA		rFH	 11.10
							,

	3250	3260	3270	3280	3290	3300	כ
CTAAATAI		ACAAAGTACG			TTGAATTATT	TG	rFH4.3
						<b>-</b> -	rFH2.7
CTAAATAI	CCATCTGGTG	ACAAAGTACG	TTATGACTGT	AATAAACCTT	TTGAATTATT	TG	rFH1.8
							rFH1.0
	3310	3320	3330	3340	3350	3360	)
GGGA AGTG		GCCAAAACGG					
		GCCAAAACGG					
SCR19							
	3370	3380	3390	3400	3410	3420	)
CAACAGGG	AAATGTGGGC	CTCCTCCACC'	TATTGACAAT	<b>GGAGACATCA</b>	CCTCCTTGTC	AT	rFH4.3
		CTCCTCCACC					
							rFH1.0
	3430	3440	3450	3460	3470	3480	)
тассаста		TATCATCAGT					
							rFH2.7
TACCAGTA	TATGCACCAT	TATCATCAGT	TGAATATCAA	TGCCAGAACT	ATTATCTACT	TA	rFH1.8
						<b>-</b> -	rFH1.0
	3490	3500	3510	3520	3530	3540	)
AGGGAAAT	TAAGATAGTAA	CATGTAGÁAA	TGGAAAGTGG	TCTCAGCCAC	CAACCTGCTT	AC	rFH4.3
							rFH2.7
AGGGAAAT	raagatagta <i>p</i>	CATGTAGAAA					
	·						rFH1.0
SCR20							_
		3560					
ATGCATG'	TGTGATACCA(	BAAGATATTAT					
ATGCATG	TGTGATACCA	GAAGATATTA:	rggaaaaaca:	TAATATAGTT(			rFH1.8

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	3610	3620	3630	3640	3650	366	0
AAAATGC	AAAGATTTA	ATTCCCAATCA	GGGGAGAATA	ATTGAATTCAT	GTGTAAACCT	GGAT	rFH4.3
							rFH2.7
AAAATGC	AAAGATTTA	ATTCCCAATCA	GGGGAGAATA	TTGAATTCAT	GTGTAAACCI	GGAT	rFH1.8
							rFH1.0
	3670		3690	3700	3710	372	
ATAGAAA	ATTCAGAGG	ATCACCTCCG			GGGTCACATC	AATT	rFH4.3
							rFH2.7
		ATCACCTCCG					rFH1.8
ATAGAAA	ATTCAGAGG	atcacctccg <sup>a</sup>	TTTCGTACAA	AGTGCATTGA	GGGTCACATC	AATT	rFH1.0
	3730		3750		3770	378	-
ATCCCAC	TTGTGTA <u>TA</u>	<u>A</u> aatcgctat	acaattatta	gtaaacctta	tggatgagaa	.atgc	rFH4.3
							rFH2.7
ATCCCAC' ATCCCAC'	TTGTGTA <u>TA</u> TTGTGTA <u>TA</u>	<u>A</u> aatcgctat <u>A</u> aatcgctat	acaattatta acaattatta	gtaaacctta gtaaacctta	tggatgagaa tggatgacac	atge	rFH1.8 rFH1.0
	3790	3800	3810	3820	3830	384	0
acatgta	tattactaa	tacagtttga	atttacattt	aaatattgtt	tagctcattt	cctc	rFH4.3
							rFH2.7
acatgta	tattactaa	atacagtttga	atttacattt	aaatattgtt	tagctcattt	cctc	rFH1.8
tttagaa	atgcacatg	gtatattacta	atacagtttg	gaatttacatt	tgaaaaa		rFH1.0
	3850	3860	3870	3880	3890	390	0
taataag	tatataaa	cttttttata	tggtggttaa	atcagtaactt	tacagactgt	tgcc	rFH4.3
							rFH2.7
taataag	tatataaa	cttttttata	itggtggtta	atcagtaactt	tacagactg	tgcc	rFH1.8
							~೯೫1 ೧

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•	3910	3920	3930	3940	3950	3960
acaaaqca	agaacattac	attcaaaact	cctaatcca	aatatgatat	gtccaagga	acaaa rFH4.3
						rFH2.7
acaaagca	agaacattac	attcaaaact	cctaatcca	aatatgatat	gtccaagga	acaaa rFH1.8
				4000		
ctatgtct	aagcaagaaa	ataaatgtta	gttcttcaa	tgtctgtttt	tattcagga	ectt rFH4.3
	aagcaagaaa					
						rFH1.0
	4020	4040	4050	4060	4070	4080
	tcttggatac					
tcagattt						rFH2.7
	tcttggatac					
						rFH1.0
	4000	43.00	4110	4120	4130	4140
				4120 acaaccaaac		
	ttcaaattag:	tattacttgo	aatacatta	acaaccaaac		
	ttcaaattag	tattacttgc	aatacatta	acaaccaaac	tatcataat	rFH4.3
actetgae	ttcaaattag  ttcaaattag	tattacttgo	aatacatta  caatacatta	acaaccaaac  acaaccaaac	tatcataat  tatcataat	rFH4.3 rFH2.7 atca rFH1.8
actetgae	ttcaaattag	tattacttgo	aatacatta  caatacatta	acaaccaaac  acaaccaaac	tatcataat  tatcataat	rFH4.3 rFH2.7 atca rFH1.8
actetgac	ttcaaattag	tattacttgc	aatacatta caatacatta caatacatta	acaaccaaac acaaccaaac	tatcataat tatcataat	rFH4.3 rFH2.7 rFH2.7 rFH1.8 rFH1.0
actetgac	ttcaaattag	tattacttgc	aatacatta caatacatta caatacatta	acaaccaaac acaaccaaac	tatcataat tatcataat	rFH4.3 rFH2.7 rFH2.7 rFH1.8 rFH1.0
actctgac	ttcaaattag	tattacttgc tattacttgc tattacttgc	aatacatta caatacatta caatacatta 4170 ctacctttgt	acaaccaaac acaaccaaac 	tatcataat tatcataat tatcataat 4190	atca rFH4.3 rFH2.7 atca rFH1.8 rFH1.0  4200 gaaag rFH4.3
actotgac	ttcaaattag	tattacttgc	aatacatta caatacatta 4170 ctacctttgt	4180	tatcataat tatcataat 4190 taaatctaac	atca rFH4.3 rFH2.7 atca rFH1.8 rFH1.0  4200 gaaag rFH4.3
caaatgta	ttcaaattag ttcaaattag ttcaaattag 4150	tattacttgc tattacttgc 4160 tactgtgtcc	4170	4180	tatcataat tatcataat tatcataat 4190 gaaatctaag	atca rFH4.3 rFH2.7 atca rFH1.8 rFH1.0  4200 gaaag rFH4.3 rFH2.7 gaaag rFH1.8
caaatgta	ttcaaattag ttcaaattag ttcaaattag 4150 atacagctaat	tattacttgc tattacttgc 4160 tactgtgtcc	4170	4180	tatcataat tatcataat tatcataat 4190 gaaatctaag	atca rFH4.3 rFH2.7 atca rFH1.8 rFH1.0  4200 gaaag rFH4.3 rFH2.7 gaaag rFH1.8
caaatgta	ttcaaattag ttcaaattag ttcaaattag 4150 atacagctaat	tattacttgc	4170	4180	tatcataat tatcataat tatcataat 4190 gaaatctaag	atca rFH4.3 rFH2.7 atca rFH1.8 rFH1.0  4200 gaaag rFH4.3 rFH2.7 gaaag rFH1.8
caaatgta	ttcaaattag	tattacttgc tattacttgc  4160 tactgtgtcc	4170 ctacctttgt	4180	tatcataat tatcataat tatcataat 4190 gaaatctaag	tatca rFH4.3 rFH2.7 tatca rFH1.8 rFH1.0  4200 gaaag rFH4.3 rFH2.7 gaaag rFH1.8 rFH1.0
caaatgta	ttcaaattag ttcaaattag ttcaaattag 4150 atacagctaat	4160 tactgtgtcccctactgtgtccc	4170 ctacctttgt	4180	tatcataat tatcataat tatcataat 4190 gaaatctaag	atca rFH4.3 rFH2.7 atca rFH1.8 rFH1.0  4200 gaaag rFH4.3 rFH2.7 gaaag rFH1.8